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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:44:36 ; Search time 146 Seconds  
(without alignments)  
413.953 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34

Sequence: 1 GGAGGUUAUACAGAGUGUUAUAGCUUACUCC 34

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptoddata/1/ina/1 COMB.seq: \*  
2: /cgn2\_6/ptoddata/1/ina/5 COMB.seq: \*  
3: /cgn2\_6/ptoddata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/ptoddata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptoddata/1/ina/H COMB.seq: \*  
6: /cgn2\_6/ptoddata/1/ina/PTUS COMB.seq: \*  
7: /cgn2\_6/ptoddata/1/ina/PP COMB.seq: \*  
8: /cgn2\_6/ptoddata/1/ina/RE COMB.seq: \*  
9: /cgn2\_6/ptoddata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	3	US-09-363-939A-93
2	34	100.0	34	3	US-09-363-939A-115
3	34	100.0	34	3	US-09-363-939A-121
4	34	100.0	34	3	US-09-363-939A-171
5	34	100.0	34	3	US-09-363-939A-172
6	34	100.0	34	3	US-09-363-939A-173
7	34	100.0	34	3	US-09-363-939A-174
8	34	100.0	34	3	US-09-363-939A-175
9	34	100.0	34	3	US-09-363-939A-176
10	34	100.0	34	3	US-09-363-939A-177
11	34	100.0	34	3	US-09-363-939A-178
12	34	100.0	34	3	US-09-363-939A-179
13	34	100.0	34	3	US-09-363-939A-180
14	34	100.0	34	3	US-09-363-939A-181
15	34	100.0	34	3	US-09-363-939A-182
16	34	100.0	34	3	US-09-363-939A-183
17	34	100.0	34	3	US-09-363-939A-184
18	34	100.0	34	3	US-09-363-939A-185
19	34	100.0	34	3	US-09-363-939A-186
20	34	100.0	34	3	US-09-791-301-93
21	34	100.0	34	3	US-09-791-301-115
22	34	100.0	34	3	US-09-791-301-121
23	34	100.0	34	3	US-09-791-301-171
24	34	100.0	34	3	US-09-791-301-172

25	34	100.0	34	3	US-09-791-301-173	Sequence 173, App
26	34	100.0	34	3	US-09-791-301-174	Sequence 174, App
27	34	100.0	34	3	US-09-791-301-175	Sequence 175, App
28	34	100.0	34	3	US-09-791-301-176	Sequence 176, App
29	34	100.0	34	3	US-09-791-301-177	Sequence 177, App
30	34	100.0	34	3	US-09-791-301-178	Sequence 178, App
31	34	100.0	34	3	US-09-791-301-179	Sequence 179, App
32	34	100.0	34	3	US-09-791-301-180	Sequence 180, App
33	34	100.0	34	3	US-09-791-301-181	Sequence 181, App
34	34	100.0	34	3	US-09-791-301-182	Sequence 182, App
35	34	100.0	34	3	US-09-791-301-183	Sequence 183, App
36	34	100.0	34	3	US-09-791-301-184	Sequence 184, App
37	34	100.0	34	3	US-09-791-301-185	Sequence 185, App
38	34	100.0	34	3	US-09-791-301-186	Sequence 186, App
39	34	100.0	34	3	US-09-363-939A-92	Sequence 92, App1
40	34	100.0	34	3	US-09-363-939A-114	Sequence 114, App
41	34	100.0	34	3	US-09-791-301-92	Sequence 92, App1
42	34	100.0	34	3	US-09-791-301-114	Sequence 114, App
43	34	100.0	34	3	US-09-363-939A-116	Sequence 116, App
44	34	100.0	34	3	US-09-791-301-116	Sequence 116, App
45	34	100.0	34	3	US-09-363-939A-91	Sequence 91, App1

#### ALIGNMENTS

RESULT 1  
US-09-363-939A-93  
; Sequence 93, Application US/09363939A  
; Patent No. 6346611  
; GENERAL INFORMATION:  
; APPLICANT: Pagratie, Nikos  
; APPLICANT: Lochrie, Michael  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
; FILE REFERENCE: Inhibitors  
; CURRENT APPLICATION NUMBER: US/09/363, 939A  
; CURRENT FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: 09/046, 247  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: 08/458, 424  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 07/714, 131  
; PRIOR FILING DATE: 1991-06-10  
; PRIOR APPLICATION NUMBER: 07/931, 473  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/964, 624  
; PRIOR FILING DATE: 1992-10-21  
; PRIOR APPLICATION NUMBER: 08/117, 991  
; PRIOR FILING DATE: 1993-09-08  
; PRIOR APPLICATION NUMBER: 07/536, 428  
; PRIOR FILING DATE: 1990-06-11  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: modified\_base  
; LOCATION: (1..(34))  
; OTHER INFORMATION: All pyrimidines are 2'F.  
US-09-363-939A-93  
Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GGAGGUUAUACAGAGUGUUAUAGCUUACUCC 34  
|||||

Db 1 GGAGGUUAVUACAGAGUCUGUAVAGCUGUACUCC 34

RESULT 2

US-09-363-939A-115

Sequence 115, Application US/09363939A

Patent No. 6346611

GENERAL INFORMATION:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

APPLICANT: Gold, Larry

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87

CURRENT APPLICATION NUMBER: US/09/363,939A

CURRENT FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10

PRIOR APPLICATION NUMBER: 07/931,473

PRIOR FILING DATE: 1992-08-17

PRIOR APPLICATION NUMBER: 07/964,624

PRIOR FILING DATE: 1992-10-21

PRIOR APPLICATION NUMBER: 08/117,991

PRIOR FILING DATE: 1993-09-08

PRIOR APPLICATION NUMBER: 07/536,428

PRIOR FILING DATE: 1990-06-11

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 115

LENGTH: 34

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

NAME/KEY: modified base

TITLE OF INVENTION: (1)..(34)

LOCATION: (1)..(34)

OTHER INFORMATION: All pyrimidines are 2'F.

US-09-363-939A-115

Query Match 100.0%; Score 34; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAVUACAGAGUCUGUAVAGCUGUACUCC 34

Db 1 GGAGGUUAVUACAGAGUCUGUAVAGCUGUACUCC 34

RESULT 3

US-09-363-939A-121

Sequence 121, Application US/09363939A

Patent No. 6346611

GENERAL INFORMATION:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

APPLICANT: Gold, Larry

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87

CURRENT APPLICATION NUMBER: US/09/363,939A

CURRENT FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10

PRIOR APPLICATION NUMBER: 07/931,473

PRIOR FILING DATE: 1992-08-17

PRIOR APPLICATION NUMBER: 07/964,624

PRIOR FILING DATE: 1992-10-21

PRIOR APPLICATION NUMBER: 08/117,991

PRIOR FILING DATE: 1993-09-08

PRIOR APPLICATION NUMBER: 07/536,428

PRIOR FILING DATE: 1990-06-11

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 121

LENGTH: 34

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

NAME/KEY: modified base

TITLE OF INVENTION: (1)..(34)

LOCATION: (1)..(34)

OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions

OTHER INFORMATION: 1-5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are

OTHER INFORMATION: 2'-OCH<sub>3</sub>; linkage at positions 34 and 35 is 3'-3'.

US-09-363-939A-121

Query Match 100.0%; Score 34; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGUUAVUACAGAGUCUGUAVAGCUGUACUCC 34

Db 1 GGAGGUUAVUACAGAGUCUGUAVAGCUGUACUCC 34

RESULT 4

US-09-363-939A-171

Sequence 171, Application US/09363939A

Patent No. 6346611

GENERAL INFORMATION:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87

CURRENT APPLICATION NUMBER: US/09/363,939A

CURRENT FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10

PRIOR APPLICATION NUMBER: 07/931,473

PRIOR FILING DATE: 1992-08-17

PRIOR APPLICATION NUMBER: 07/964,624

PRIOR FILING DATE: 1992-10-21

PRIOR APPLICATION NUMBER: 08/117,991

PRIOR FILING DATE: 1993-09-08

PRIOR APPLICATION NUMBER: 07/536,428

PRIOR FILING DATE: 1990-06-11

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 171

LENGTH: 34

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

NAME/KEY: modified base

TITLE OF INVENTION: (1)..(34)

LOCATION: (1)..(34)

OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions

OTHER INFORMATION: 1-5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are

OTHER INFORMATION: 2'-OCH<sub>3</sub>; linkage at positions 34 and 35 is 3'-3'.

US-09-363-939A-171

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Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34
      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

Db      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 5
US-09-363-939A-172
; Sequence 172, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 172
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'OH3;
; OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-172

Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34
      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

Db      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 6
US-09-363-939A-173
; Sequence 173, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
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; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 173
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 1-4 are 2'OH3; linkage at positions 34 and 35 is
; OTHER INFORMATION: 3'-3'.
US-09-363-939A-173

Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34
      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

Db      1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 7
US-09-363-939A-174
; Sequence 174, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)-(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 5, 6, and 11 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
```

```
US-09-363-939A-174
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
      |||
Db      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
```

```
RESULT 8
US-09-363-939A-175
; Sequence 175, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)-(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a' and g's at positions
; OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
; OTHER INFORMATION: 18 3'-3'.
```

```
US-09-363-939A-175
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
      |||
Db      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
```

```
RESULT 9
US-09-363-939A-176
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; Sequence 176, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)-(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 20, 22 and 24 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
```

```
US-09-363-939A-176
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
      |||
Db      1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
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```
RESULT 10
US-09-363-939A-177
; Sequence 177, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
```

```

; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 25, 28 and 30 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
US-09-363-939A-177

Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 11
US-09-363-939A-178
; Sequence 178, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; g at position 20 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-178

Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 12
US-09-363-939A-179
; Sequence 179, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a at position 22 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-179

Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 13
US-09-363-939A-180
; Sequence 180, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
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; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a at position 24 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-180
```

```

Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
```

```

RESULT 14
US-09-363-939A-181
; Sequence 181, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
; OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-182
```

```

; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 1-5, 8, 11, 25 and 30 are 2'-OCH3; linkage at
; OTHER INFORMATION: positions 34 and 35 is 3'-3'.
US-09-363-939A-181

Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 15
US-09-363-939A-182
; Sequence 182, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
; OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-363-939A-182
```

```

Qy      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db      1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
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Search completed: December 27, 2005, 16:45:24
Job time : 146 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:58:35 / Search time 815 Seconds  
(without alignments)  
344.980 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34  
Sequence: 1 ggaagguuauacagagucguuagucguacucc 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA Main:  
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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCONB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCONB.seq:\*  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCONB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	34	100.0	34	US-09-791-301-93
2	34	100.0	34	US-09-791-301-115
3	34	100.0	34	US-09-791-301-121
4	34	100.0	34	US-09-791-301-171
5	34	100.0	34	US-09-791-301-172
6	34	100.0	34	US-09-791-301-173
7	34	100.0	34	US-09-791-301-174
8	34	100.0	34	US-09-791-301-175
9	34	100.0	34	US-09-791-301-176
10	34	100.0	34	US-09-791-301-177
11	34	100.0	34	US-09-791-301-178
12	34	100.0	34	US-09-791-301-179
13	34	100.0	34	US-09-791-301-180
14	34	100.0	34	US-09-791-301-181
15	34	100.0	34	US-09-791-301-182
16	34	100.0	34	US-09-791-301-183
17	34	100.0	34	US-09-791-301-184
18	34	100.0	34	US-09-791-301-185
19	34	100.0	34	US-09-791-301-186
20	34	100.0	34	US-10-718-833-12
21	34	100.0	34	US-10-762-915-1
22	34	100.0	34	US-10-762-915-2
23	34	100.0	34	US-10-762-915-3

24	34	100.0	34	US-10-762-915-6	Sequence 6, Appl
25	34	100.0	34	US-10-762-915-7	Sequence 7, Appl
26	34	100.0	34	US-10-762-915-8	Sequence 8, Appl
27	34	100.0	34	US-10-762-915-21	Sequence 21, Appl
28	34	100.0	34	US-10-762-915-22	Sequence 22, Appl
29	34	100.0	34	US-10-762-915-27	Sequence 27, Appl
30	34	100.0	34	US-10-762-915-148	Sequence 148, Appl
31	34	100.0	34	US-10-812-642-93	Sequence 93, Appl
32	34	100.0	34	US-10-812-642-115	Sequence 115, Appl
33	34	100.0	34	US-10-812-642-121	Sequence 121, Appl
34	34	100.0	34	US-10-812-642-171	Sequence 171, Appl
35	34	100.0	34	US-10-812-642-172	Sequence 172, Appl
36	34	100.0	34	US-10-812-642-173	Sequence 173, Appl
37	34	100.0	34	US-10-812-642-174	Sequence 174, Appl
38	34	100.0	34	US-10-812-642-175	Sequence 175, Appl
39	34	100.0	34	US-10-812-642-176	Sequence 176, Appl
40	34	100.0	34	US-10-812-642-177	Sequence 177, Appl
41	34	100.0	34	US-10-812-642-178	Sequence 178, Appl
42	34	100.0	34	US-10-812-642-179	Sequence 179, Appl
43	34	100.0	34	US-10-812-642-180	Sequence 180, Appl
44	34	100.0	34	US-10-812-642-181	Sequence 181, Appl
45	34	100.0	34	US-10-812-642-182	Sequence 182, Appl

#### ALIGNMENTS

RESULT 1  
US-09-791-301-93  
Sequence 93, Application US/09791301  
Publication No. US2003006493A1  
GENERAL INFORMATION:  
APPLICANT: Patratia, Mike  
APPLICANT: Lech, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 93  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
NAME/KEY: modified base  
LOCATION: (1)..(34)  
OTHER INFORMATION: All pyrimidines are 2'F.  
US-09-791-301-93  
Query Match 100.0%, Score 34, DB 3, Length 34;  
Best Local Similarity 100.0%, Pred. No. 2.8e-05;  
Matches 34, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 GGAGGUTUATUACAGAGUCUGUATAGCUGUATCC 34  
DB 1 GGAGGUTUATUACAGAGUCUGUATAGCUGUATCC 34

## RESULT 2

```

US-09-791-301-115
Sequence 115, Application US/09791301
Publication No. US20030064963A1
GENERAL INFORMATION:
APPLICANT: Pagratis, Nikos
APPLICANT: Lochrie, Michael
APPLICANT: Gold, Larry
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: NEX 87/c
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIORITY APPLICATION NUMBER: 09/046,247
PRIORITY FILING DATE: 1998-03-23
PRIORITY APPLICATION NUMBER: 08/458,424
PRIORITY FILING DATE: 1995-06-02
PRIORITY APPLICATION NUMBER: 07/714,131
PRIORITY FILING DATE: 1991-06-10
PRIORITY APPLICATION NUMBER: 07/931,473
PRIORITY FILING DATE: 1992-08-17
PRIORITY APPLICATION NUMBER: 07/964,624
PRIORITY FILING DATE: 1992-10-21
PRIORITY APPLICATION NUMBER: 08/117,991
PRIORITY FILING DATE: 1993-09-08
PRIORITY APPLICATION NUMBER: 07/536,428
PRIORITY FILING DATE: 1990-06-11
PRIORITY APPLICATION NUMBER: 09/363,939
PRIORITY FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 115
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: modified base
LOCATION: (1) ..(34)
OTHER INFORMATION: All pyrimidines are 2'F.
US-09-791-301-115

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Query Match	100.0%	Score 34	DB 3	Length 34
Best Local Similarity	100.0%	Pred. No. 2.8e-05		
Matches	34	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	1	GGAGGTUAVUACAGAGUCUCGUUAGUCUGACATCC	34	
Db	1	GGAGGTUAVUACAGAGUCUCGUUAGUCUGACATCC	34	

### RESULT 3

US-09-791-301-121  
Sequence 121, Application US/09791301  
Publication No. US20030064943A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23

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1      PRIOR APPLICATION NUMBER: 08/458,424
2      PRIOR FILING DATE: 1995-06-02
3      PRIOR APPLICATION NUMBER: 07/714,131
4      PRIOR FILING DATE: 1991-06-10
5      PRIOR APPLICATION NUMBER: 07/931,473
6      PRIOR FILING DATE: 1992-08-17
7      PRIOR APPLICATION NUMBER: 07/964,624
8      PRIOR FILING DATE: 1992-10-21
9      PRIOR APPLICATION NUMBER: 08/117,991
10     PRIOR FILING DATE: 1993-09-08
11     PRIOR APPLICATION NUMBER: 07/536,428
12     PRIOR FILING DATE: 1990-06-11
13     PRIOR APPLICATION NUMBER: 09/363,939
14     PRIOR FILING DATE: 1999-07-29
15     NUMBER OF SEQ ID NOS: 216
16     SOFTWARE: PatentIn Ver. 2.0
17     SEQ ID NO 121
18     LENGTH: 34
19     TYPE: RNA
20     ORGANISM: Artificial Sequence
21     FEATURES:
22     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
23     OTHER INFORMATION: Sequence
24     NAME/KEY: modified base
25     LOCATION: (1) .. (34)
26     OTHER INFORMATION: All pyrimidines are 2'.F.
27     US-09-791-301-121

```

Query Match	100.0%	Score 34	DB 3	length 34
Best Local Similarity	100.0%	Pred. No.	2.8e-05	
Matches 34	Conservative 0	Mismatches 0	Indels 0	Gaps 0

RESULTS 4  
HS-09-791-301-171

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1 / Sequence 171, Application US/09791301
2 / Publication No. US20030064943A1
3 /
4 / GENERAL INFORMATION:
5 / APPLICANT: Pagratis, Nikos
6 / APPLICANT: Lochrie, Michael
7 / APPLICANT: Gold, Larry
8 / TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
9 / TITLE OF INVENTION: Inhibitors
10 /
11 / FILE REFERENCE: NEX 87/C
12 / CURRENT APPLICATION NUMBER: US/09/791,301
13 / CURRENT FILING DATE: 2001-02-23
14 / PRIOR APPLICATION NUMBER: 09/046,247
15 / PRIOR FILING DATE: 1998-03-23
16 / PRIOR APPLICATION NUMBER: 08/458,424
17 / PRIOR FILING DATE: 1995-06-02
18 / PRIOR APPLICATION NUMBER: 07/114,131
19 / PRIOR FILING DATE: 1991-06-10
20 / PRIOR APPLICATION NUMBER: 07/931,473
21 / PRIOR FILING DATE: 1992-08-17
22 / PRIOR APPLICATION NUMBER: 07/964,624
23 / PRIOR FILING DATE: 1992-10-21
24 / PRIOR APPLICATION NUMBER: 08/117,991
25 / PRIOR FILING DATE: 1993-09-08
26 / PRIOR APPLICATION NUMBER: 07/936,428
27 / PRIOR FILING DATE: 1990-06-11
28 / PRIOR APPLICATION NUMBER: 09/363,939
29 / PRIOR FILING DATE: 1999-07-29
30 / NUMBER OF SEQ ID NOS: 216
31 / SOFTWARE: PatentIn Ver. 2.0
32 /
33 / SEQ ID NO 171
34 / LENGTH: 34
35 / TYPE: RNA
36 / ORGANISM: Artificial Sequence
37 / FEATURE:

```



OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Sequence  
NAME/KEY: modified base  
LOCATION: (1)..(34)  
OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions  
OTHER INFORMATION: 1-5, 8, 11, 13-16, 20, 22, 24-25, 28 and 30 are  
OTHER INFORMATION: 2'-OCH<sub>3</sub>; linkage at positions 34 and 35 is 3'-3'.  
US-09-791-301-171

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34  
Db 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

## RESULT 5

US-09-791-301-172  
Sequence 172, Application US/09791301  
Publication No. US20030064943A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 172  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Sequence  
NAME/KEY: modified base  
LOCATION: (1)..(34)  
OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions  
OTHER INFORMATION: 11, 13-16, 20, 22, 24-25, 28 and 30 are 2'OCH<sub>3</sub>;  
OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.  
US-09-791-301-172

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34  
Db 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

## RESULT 6

US-09-791-301-173  
Sequence 173, Application US/09791301  
Publication No. US20030064943A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 173  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Sequence  
NAME/KEY: modified base  
LOCATION: (1)..(34)  
OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions  
OTHER INFORMATION: 1-4 are 2'OCH<sub>3</sub>; linkage at positions 34 and 35 is  
OTHER INFORMATION: 3'-3'.  
US-09-791-301-173

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34  
Db 1 GGAGGUUUAUACAGAGUCUGUUAUAGCUGUACUCC 34

## RESULT 7

US-09-791-301-174  
Sequence 174, Application US/09791301  
Publication No. US20030064943A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473

```

; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
; OTHER INFORMATION: 5, 8, and 11 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-174
```

```
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
Db      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
```

#### RESULT 8

```
US-09-791-301-175
; Sequence 175, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US/09/791,301
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
```

```

; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a' and g's at positions
; OTHER INFORMATION: 13-16 are 2'-OCH3; linkage at positions 34 and 35
; OTHER INFORMATION: is 3'-3'.
US-09-791-301-175
```

```
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
Db      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
```

#### RESULT 9

```
US-09-791-301-176
; Sequence 176, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US/09/791,301
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions
; OTHER INFORMATION: 20, 22 and 24 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-176
```

```
Query Match          100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
Db      1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34
```

#### RESULT 10

```
US-09-791-301-177
; Sequence 177, Application US/09791301
; Publication No. US20030064943A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 177
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 25, 28 and 30 are 2'-OCH3; linkage at positions 34
; OTHER INFORMATION: and 35 is 3'-3'.
US-09-791-301-177

Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGAGGUUUAUACAGAGUCUGUUAAGCUGUACUCC 34
Db      1  GGAGGUUUAUACAGAGUCUGUUAAGCUGUACUCC 34

RESULT 11
US-09-791-301-178
; Sequence 178, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a at position 22 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-179
```

```

; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 178
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, g at position 20 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-178

Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGAGGUUUAUACAGAGUCUGUUAAGCUGUACUCC 34
Db      1  GGAGGUUUAUACAGAGUCUGUUAAGCUGUACUCC 34

RESULT 12
US-09-791-301-179
; Sequence 179, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a at position 22 is
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-179
```

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

## RESULT 13

US-09-791-301-180  
; Sequence 180, Application US/09791301  
; Publication No. US20030064943A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagratzis, Nikos  
; APPLICANT: Lochrie, Michael  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE: NEX 87/C  
; CURRENT APPLICATION NUMBER: US/09/791,301  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/046,247  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: 08/458,424  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 07/714,131  
; PRIOR FILING DATE: 1991-06-10  
; PRIOR APPLICATION NUMBER: 07/931,473  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/964,624  
; PRIOR FILING DATE: 1992-10-21  
; PRIOR APPLICATION NUMBER: 08/117,991  
; PRIOR FILING DATE: 1993-09-08  
; PRIOR APPLICATION NUMBER: 07/536,428  
; PRIOR FILING DATE: 1990-06-11  
; PRIOR APPLICATION NUMBER: 09/363,939  
; PRIOR FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 180  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: modified base  
; LOCATION: (1)..(34)  
; OTHER INFORMATION: All pyrimidines are 2'F; a at position 24 is  
; OTHER INFORMATION: 2'-OCH3; linkage at positions 34 and 35 is 3'-3'.  
US-09-791-301-180

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 14

US-09-791-301-181  
; Sequence 181, Application US/09791301  
; Publication No. US20030064943A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagratzis, Nikos  
; APPLICANT: Lochrie, Michael  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: NEX 87/C  
; CURRENT APPLICATION NUMBER: US/09/791,301  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/046,247  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: 08/458,424  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 07/714,131  
; PRIOR FILING DATE: 1991-06-10  
; PRIOR APPLICATION NUMBER: 07/931,473  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/964,624  
; PRIOR FILING DATE: 1992-10-21  
; PRIOR APPLICATION NUMBER: 08/117,991  
; PRIOR FILING DATE: 1993-09-08  
; PRIOR APPLICATION NUMBER: 07/536,428  
; PRIOR FILING DATE: 1990-06-11  
; PRIOR APPLICATION NUMBER: 09/363,939  
; PRIOR FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 181  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: modified base  
; LOCATION: (1)..(34)  
; OTHER INFORMATION: All pyrimidines are 2'F; a's and g's at positions  
; OTHER INFORMATION: 1-5, 8, 11, 25 and 30 are 2'-OCH3; linkage at  
; OTHER INFORMATION: positions 34 and 35 is 3'-3'.  
US-09-791-301-181

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 15

US-09-791-301-182  
; Sequence 182, Application US/09791301  
; Publication No. US20030064943A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagratzis, Nikos  
; APPLICANT: Lochrie, Michael  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE: NEX 87/C  
; CURRENT APPLICATION NUMBER: US/09/791,301  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/046,247  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: 08/458,424  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 07/714,131  
; PRIOR FILING DATE: 1991-06-10  
; PRIOR APPLICATION NUMBER: 07/931,473  
; PRIOR FILING DATE: 1992-08-17  
; PRIOR APPLICATION NUMBER: 07/964,624  
; PRIOR FILING DATE: 1992-10-21  
; PRIOR APPLICATION NUMBER: 08/117,991  
; PRIOR FILING DATE: 1993-09-08  
; PRIOR APPLICATION NUMBER: 07/536,428  
; PRIOR FILING DATE: 1990-06-11  
; PRIOR APPLICATION NUMBER: 09/363,939  
; PRIOR FILING DATE: 1999-07-29

```
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 182
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(34)
; OTHER INFORMATION: All pyrimidines are 2'F, a's and g's at positions
; OTHER INFORMATION: 1-5, 8, 11, 13-16, 24-25, 28 and 30 are 2'-OCH3;
; OTHER INFORMATION: linkage at positions 34 and 35 is 3'-3'.
US-09-791-301-182

Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAGGUUAUUCAGAGUCUGUAUAGCUGUACUCC 34
Db      1 GGAGGUUAUUCAGAGUCUGUAUAGCUGUACUCC 34
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Search completed: December 27, 2005, 16:59:16  
Job time : 816 secs

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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 15:06:46 / Search time 296 Seconds  
(without alignments)  
59.610 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34  
Sequence: 1 ggaaguuuacagagucguuagcugacucc 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Published Applications NA New:

1: /cgn2\_6/prodata/2/pubpna/US08 NEW PUB.seq:\*  
2: /cgn2\_6/prodata/2/pubpna/US06 NEW PUB.seq:\*  
3: /cgn2\_6/prodata/2/pubpna/US07 NEW PUB.seq:\*  
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5: /cgn2\_6/prodata/2/pubpna/US09 NEW PUB.seq:\*  
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8: /cgn2\_6/prodata/2/pubpna/US11 NEW PUB.seq2:\*  
9: /cgn2\_6/prodata/2/pubpna/US11 NEW PUB.seq3:\*  
10: /cgn2\_6/prodata/2/pubpna/US60\_NEW PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	59.4	150481	7	US-11-112-908-37
2	20.2	59.4	171162	7	US-11-112-908-38
3	19.2	56.5	691	6	US-10-750-185-64880
4	19.2	56.5	2279	6	US-10-750-185-57144
5	18.6	54.7	971	6	US-10-750-185-62416
6	18.6	54.7	1537	6	US-10-750-185-33471
7	18.4	54.1	1086	6	US-10-750-185-51403
8	18.2	53.5	25	7	US-11-121-086-617034
9	18.2	53.5	435	6	US-10-467-657-263
10	18.2	53.5	435	6	US-10-467-657-3599
11	18.2	53.5	1671	6	US-10-750-185-56074
12	18.2	53.5	1894	6	US-10-995-561-248
13	18.2	53.5	2439	6	US-10-995-561-249
14	18.2	53.5	2789	6	US-10-995-561-250
15	18.2	53.5	20991	6	US-10-995-561-13488
16	18.2	53.5	31657	6	US-10-995-561-13334
17	18.2	53.5	33175	6	US-10-995-561-13270
18	18.2	53.5	5134	7	US-11-060-005-1
19	18.2	52.9	6160	7	US-11-060-005-3
20	18.2	52.9	148220	7	US-11-121-086-90
21	18.2	52.9	207600	7	US-11-112-908-31
22	17.8	52.4	201	6	US-10-995-561-53373
23	17.8	52.4	201	6	US-10-995-561-74017

24	17.8	52.4	598	6	US-10-750-185-769	Sequence 769, App
25	17.8	52.4	819	6	US-10-793-626-3197	Sequence 3197, Ap
26	17.8	52.4	3344	6	US-10-793-626-3567	Sequence 3567, Ap
27	17.8	52.4	13395	6	US-10-995-561-13452	Sequence 13452, A
28	17.8	52.4	35101	6	US-10-995-561-13315	Sequence 13315, A
29	17.6	51.8	367	8	US-11-132-285-57	Sequence 57, Appl
30	17.6	51.8	1000	6	US-10-750-185-26175	Sequence 26175, A
31	17.6	51.8	1081	6	US-10-750-185-54369	Sequence 54369, A
32	17.6	51.8	1322	6	US-10-750-185-41390	Sequence 41390, A
33	17.6	51.8	2303	6	US-10-750-185-36421	Sequence 36421, A
34	17.6	51.8	179777	7	US-11-121-086-106	Sequence 106, App
35	17.4	51.2	1087	6	US-10-750-185-42060	Sequence 42060, A
36	17.4	51.2	1485	6	US-10-750-185-41900	Sequence 41900, A
37	17.4	51.2	1524	6	US-10-750-185-42660	Sequence 42660, A
38	17.4	51.2	2482	6	US-10-750-185-42895	Sequence 42895, A
39	17.4	51.2	2926	6	US-10-750-185-48539	Sequence 48539, A
40	17.4	51.2	2387	6	US-10-793-626-4367	Sequence 4367, Ap
41	17.4	51.2	3137	6	US-10-793-626-3842	Sequence 3842, Ap
42	17.4	51.2	3569	6	US-10-793-626-4443	Sequence 4443, Ap
43	17.4	51.2	4297	6	US-10-793-626-4092	Sequence 4092, Ap
44	17.4	51.2	150314	7	US-11-112-908-24	Sequence 24, Appl
45	17.4	51.2	156544	7	US-11-121-086-81	Sequence 81, Appl

## ALIGNMENTS

```

RESULT 1
US-11-112-908-37/c
/ Sequence 37, Application US/11112908
/ Publication No. US20050260659A1
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Lisa M.
/ TITLE OF INVENTION: Breast Cancer Biomarkers
/ FILE REFERENCE: 04-164-US
/ CURRENT APPLICATION NUMBER: US/11/112,908
/ CURRENT FILING DATE: 2005-04-22
/ PRIOR APPLICATION NUMBER: US 60/564,758
/ PRIOR FILING DATE: 2004-04-23
/ PRIOR APPLICATION NUMBER: US 60/575,978
/ PRIOR FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US 60/531,702
/ PRIOR FILING DATE: 2004-11-30
/ PRIOR APPLICATION NUMBER: US 60/533,826
/ PRIOR FILING DATE: 2004-12-07
/ NUMBER OF SEQ ID NOS: 511
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37
/ LENGTH: 150481
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-112-908-37

Query Match          59.4%; Score 20.2; DB 7; Length 150481;
Best Local Similarity 48.5%; Pred. No. 14;
Matches 16; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY      1 ggaaguuuacagagucguuagcugacucc 33
Db      67191 gTAAgATTtTACAGAGCTTTATGACATTATGTC 67159

RESULT 2
US-11-112-908-38/c
/ Sequence 38, Application US/11112908
/ Publication No. US20050260659A1
/ GENERAL INFORMATION:
/ APPLICANT: Harris, Cole
/ TITLE OF INVENTION: Breast Cancer Biomarkers
/ FILE REFERENCE: 04-164-US
/ CURRENT APPLICATION NUMBER: US/11/112,908

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```

; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

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Query Match      59.4%; Score 20.2; DB 7; Length 171162;
Best Local Similarity 48.5%; Pred. No. 14;
Matches 16; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1 GGAGUUUACAGUCUGUUAUAGCUCU 33
Db      133691 GTAAAGTATTACAGAGCTTTATGACATTAGTC 133659

```

```

RESULT 3
US-10-750-185-64880
; Sequence 64880, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64880
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Bovine 19866881409947
US-10-750-185-64880

```

```

Query Match      56.5%; Score 19.2; DB 6; Length 691;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 12; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      6 UUAUUAACAGUCUGUUAUAGCUCU 29
Db      450 TCATTACAGGCTCTGTATTAGTTGT 473

```

```

RESULT 4
US-10-750-185-57144/c
; Sequence 57144, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis

```

```

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57144
; LENGTH: 2279
; TYPE: DNA
; ORGANISM: Bovine 19866880808150
US-10-750-185-57144

```

```

Query Match      56.5%; Score 19.2; DB 6; Length 2279;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1 GGAGUUUACAGUCUGUUAUAGCUCU 32
Db      125 GGCTTTACTGCGAGAGCTGGAATGCTGCCCT 94

```

```

RESULT 5
US-10-750-185-62416/c
; Sequence 62416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62416
; LENGTH: 971
; TYPE: DNA
; ORGANISM: Bovine 19866880400331
US-10-750-185-62416

```

```

Query Match      54.7%; Score 18.6; DB 6; Length 971;
Best Local Similarity 56.0%; Pred. No. 26;
Matches 14; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      10 UACAGAGUCUGUUAUAGCUCUCC 34
Db      173 TACAGAGTCAGTTAGCTGTAGTAC 149

```

```

RESULT 6
US-10-750-185-33471
; Sequence 33471, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185

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/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 33471
/ LENGTH: 1527
/ TYPE: DNA
/ ORGANISM: Bovine 1986680240664
US-10-750-185-33471
```

```
Query Match 54.7%; Score 18.6; DB 6; Length 1527;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 15; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy 1 GGAGCUUUAUACGAGUCUUAUAGCUCUC 33
Db 299 GGACTTTCTACAGCTTCTTATACCTGAATC 331
```

```
RESULT 7
US-10-750-185-51403/c
/ Sequence 51403, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 51403
/ LENGTH: 1086
/ TYPE: DNA
/ ORGANISM: Bovine 1986680936749
US-10-750-185-51403
```

```
Query Match 54.1%; Score 18.4; DB 6; Length 1086;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 GGAGCUUUAUACGAGUCUUAUAGCUC 28
Db 1042 GGAGCAGTTTACAGAGTCAGATTGCTG 1015
```

```
RESULT 8
US-11-121-849-617034/c
/ Sequence 617034, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray probe Sequence Listing Generator V 1.1
/ SEQ ID NO 617034
/ LENGTH: 25
/ TYPE: DNA
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```
/ ORGANISM: Homo sapien
US-11-121-849-617034
```

```
Query Match 53.5%; Score 18.2; DB 7; Length 25;
Best Local Similarity 56.5%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 9 UUAACAGUCUCUUAUAGCUCUAC 31
Db 24 TTGAGAGTGTCATGCTGTAC 2
```

```
RESULT 9
US-10-467-657-263
/ Sequence 263, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 263
/ LENGTH: 435
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-263
```

```
Query Match 53.5%; Score 18.2; DB 6; Length 435;
Best Local Similarity 48.4%; Pred. No. 34;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 4 GGUUAUUAACAGAGUCUUAUAGCUCGAC 34
Db 402 GATTATCAAAAGTATGAAGAAGTGTATCC 432
```

```
RESULT 10
US-10-467-657-3599
/ Sequence 3599, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 3599
/ LENGTH: 435
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3599
```

```
Query Match 53.5%; Score 18.2; DB 6; Length 435;
Best Local Similarity 48.4%; Pred. No. 34;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
```

QY 4 GGUAUUACAGUCUGUUAUAGCUGUACUCC 34  
Db 402 GATTATCAAGACTATGACAGACTGACTCC 432

RESULT 11  
US-10-750-185-56074/c  
; Sequence 56074, Application US/10750185  
; Publication No. US200502603A1  
; GENERAL INFORMATION:  
; APPLICANT: NMT GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MW1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56074  
; LENGTH: 1671  
; TYPE: DNA  
; ORGANISM: Bovine 19866881576202  
US-10-750-185-56074

Query Match 53.5%; Score 18.2; DB 6; Length 1671;  
Best Local Similarity 60.3%; Pred. No. 44;  
Matches 14; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGUCUGUUAUAGCUGUAC 23  
Db 365 GGAGGTATTACAGACTGACTGAT 343

RESULT 12  
US-10-995-561-248  
; Sequence 248, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 248  
; LENGTH: 1894  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-248

Query Match 53.5%; Score 18.2; DB 6; Length 1894;  
Best Local Similarity 58.1%; Pred. No. 45;  
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGUCUGUUAUAGCUGUAC 31  
Db 169 GGGTGTCATTACAGACCTGAAAAAAGTGGAC 199

RESULT 13  
US-10-995-561-249  
; Sequence 249, Application US/10995561  
; Publication No. US20050272054A1

; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 249  
; LENGTH: 2439  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-249

Query Match 53.5%; Score 18.2; DB 6; Length 2439;  
Best Local Similarity 58.1%; Pred. No. 48;  
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGUCUGUUAUAGCUGUAC 31  
Db 974 GGGTGTCATTACAGACCTGAAAAAAGTGGAC 1004

RESULT 14  
US-10-995-561-250  
; Sequence 250, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 250  
; LENGTH: 2789  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-250

Query Match 53.5%; Score 18.2; DB 6; Length 2789;  
Best Local Similarity 58.1%; Pred. No. 49;  
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGUCUGUUAUAGCUGUAC 31  
Db 974 GGGTGTCATTACAGACCTGAAAAAAGTGGAC 1004

RESULT 15  
US-10-995-561-13488/c  
; Sequence 13488, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13488  
; LENGTH: 20991  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-13488

Query Match 53.5%; Score 18.2; DB 6; Length 20991;  
Best Local Similarity 58.1%; Pred. No. 75;  
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGAGGUAUUACAGAGUCUGUAUAGCUGUAC 31  
|||:|||||:|:|:|  
Db 77 GGAGGUAUUACAGAGUCUGUAUAGCUGUAC 47

Search completed: December 27, 2005, 17:04:24  
Job time : 297 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 13:28:20 : Search time 1988 Seconds  
(without alignments)  
972.172 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34  
Sequence: 1 GAGGGUUAUACAGAGUCUGUAAGUCUGUACUCC 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_in:\*
- 3: gb\_env:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pr:\*
- 9: gb\_ro:\*
- 10: gb\_scb:\*
- 11: gb\_ey:\*
- 12: gb\_un:\*
- 13: gb\_vl:\*
- 14: gb\_hcg:\*
- 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	AR193289 Sequence
2	34	100.0	34	6	AR193311 Sequence
3	34	100.0	34	6	AR193317 Sequence
4	34	100.0	34	6	AR193361 Sequence
5	34	100.0	34	6	AR193362 Sequence
6	34	100.0	34	6	AR193363 Sequence
7	34	100.0	34	6	AR193364 Sequence
8	34	100.0	34	6	AR193365 Sequence
9	34	100.0	34	6	AR193366 Sequence
10	34	100.0	34	6	AR193367 Sequence
11	34	100.0	34	6	AR193368 Sequence
12	34	100.0	34	6	AR193369 Sequence
13	34	100.0	34	6	AR193370 Sequence
14	34	100.0	34	6	AR193371 Sequence
15	34	100.0	34	6	AR193372 Sequence
16	34	100.0	34	6	AR193373 Sequence
17	34	100.0	34	6	AR193374 Sequence
18	34	100.0	34	6	AR193375 Sequence

19	34	100.0	34	6	AR193376 Sequence
20	34	100.0	34	6	AR491289 Sequence
21	34	100.0	34	6	AR491311 Sequence
22	34	100.0	34	6	AR491317 Sequence
23	34	100.0	34	6	AR491361 Sequence
24	34	100.0	34	6	AR491362 Sequence
25	34	100.0	34	6	AR491363 Sequence
26	34	100.0	34	6	AR491364 Sequence
27	34	100.0	34	6	AR491365 Sequence
28	34	100.0	34	6	AR491366 Sequence
29	34	100.0	34	6	AR491367 Sequence
30	34	100.0	34	6	AR491368 Sequence
31	34	100.0	34	6	AR491369 Sequence
32	34	100.0	34	6	AR491370 Sequence
33	34	100.0	34	6	AR491371 Sequence
34	34	100.0	34	6	AR491372 Sequence
35	34	100.0	34	6	AR491373 Sequence
36	34	100.0	34	6	AR491374 Sequence
37	34	100.0	34	6	AR491375 Sequence
38	34	100.0	34	6	AR491376 Sequence
39	34	100.0	34	6	AR193288 Sequence
40	34	100.0	36	6	AR193310 Sequence
41	34	100.0	36	6	AR491288 Sequence
42	34	100.0	36	6	AR491310 Sequence
43	34	100.0	37	6	AR193312 Sequence
44	34	100.0	37	6	AR491312 Sequence
45	34	100.0	43	6	AR193287 Sequence

## ALIGNMENTS

RESULT 1	AR193289	34 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193289	Sequence 93 from patent US 6346611.			
DEFINITION	AR193289				
ACCESSION	AR193289				
VERSION	AR193289.1	GI:20239254			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 34)				
AUTHORS	Pagratie,N., Lochrie,M. and Gold,L.				
TITLE	High affinity TGF-beta, nucleic acid ligands and inhibitors				
JOURNAL	Patent: US 6346611-A 93 12-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..34				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 34;	DB 6;	Length 34;		
Best Local Similarity	67.6%; Pred. No. 0.00024;				
Matches	23; Conservative 11; Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1 GAGGGUUAUACAGAGUCUGUAAGUCUGUACUCC 34				
Db	1 GAGGTTATTACAGAGCTGTATAGCTGTACTCC 34				
RESULT 2	AR193311	34 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193311	Sequence 115 from patent US 6346611.			
DEFINITION	AR193311				
ACCESSION	AR193311				
VERSION	AR193311.1	GI:20239276			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 34)				
AUTHORS	Pagratie,N., Lochrie,M. and Gold,L.				

TITLE	High affinity TGF.beta. nucleic acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 115 12-EEB-2002;
FEATURES	Location/Qualifiers
SOURCE	1. .34

**ORIGIN**

Query Match 100.0%; Score 34; DB 6; Length 34;  
 Best Local Similarity 67.6%; Pred. No. 0.00024;  
 Matches 23; Conservative 11; Mismatches 0; Gaps 0;

Qy 1 GGAGGUAUAACAGAGUCUCUGUAUAGCUCGUACUCC 34  
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Db 1 GGAGGTTATTACAGAGCTGTGTATGACTGACTCC 34

RESULT 3			
ARI93317			
LOCUS	ARI93317	34 bp	DNA
DEFINITION	Sequence 121 from patent US 6346611.		linear
			PAT 20-APR-2002

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/organism="unknown"
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Query Match	100.0%	Score 34	DB 6	Length 34
Best Local Similarity	67.6%	Pred. No. 0.00024		
Matches 23	Conservative 11	Mismatches 0	Indels 0	Gaps 0

RESULT 4			
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LOCUS	AR193361	34 bp	DNA
DEFINITION	Sequence 171 from patent US 6346611.		linear PAT 20-APR-2002

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/organism="unknown"
/mol_type="unassigned DNA"

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 Db 1 GGAGGTTATTACAGAGCTGTATTAGCTGTACTCC 34

	RESULT	5			
ARI93362	LOCUS	ARI93362	34 bp	DNA	linear
DEFINITION	Sequence	172 from patent US 634611.		PAT 20-APR-2002	
ACCESSION	ARI93362				
VERSION	ARI93362.1	GI:20239327			

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/organism="unknown"
/mol_type="unassigned DNA"

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QY	Db
1 GGAGGUAUUA CAGAGUCGUUAUAGCUUACUC 34	1 GGAGGUAUUA CAGAGUCGUUAUAGCUUACUC 34
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LOCUS	AR193363	34 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 173 from patent US 6346611.				
ACCESSION	AR193363				
VERSION	AR193363.1	GI:20239328			

TITLE	High affinity TGF-beta nuclear acid ligands and inhibitors
JOURNAL	Patent: US 6346611-A 173 12-FEB-2002;
FEATURES	Location/Qualifiers
SOURCE	1. .34

Qy 1 GGAAGTUUUACAGAGUCUGUAUAGCUGUACUCC 34  
|||:::|||||:::|||||:::|||||  
Db 1 GGAAGTTATTACAGAGCTGTATTAGCTGACTCC 34

RESULT 7			
AR193364			
LOCUS	AR193364	34 bp	DNA
DEFINITION	Sequence 174 from patent US 6346611.		Linear
			PAT 20-APR-2002

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 34)	Pagratzis, N., Lochrie, M. and Gold, L.	High affinity TGF. beta. nucleic acid ligands and inhibitors

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (pages 1 to 34)  
Pagratidis, N., Lochrie, M. and Gold, L.  
High affinity TGF-beta<sub>1</sub> nucleic acid ligands and inhibitors  
Patent: US 6346611-A 179 12-FEB-2002;

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FEATURES
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    Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"
ORIGIN
  Query Match
    100.0%; Score 34; DB 6; Length 34;
  Best Local Similarity
    67.6%; Pred. No. 0.00024;
  Matches
    23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY
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  |||||:::|||||:::|||||:::|||||:::|||||
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34

RESULT 13
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  DEFINITION
    Sequence 180 from patent US 6346611.
  ACCESSION
    AR193370
  VERSION
    AR193370.1 GI:20239335
  KEYWORDS
    '
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 34)
    Pagratia,N., Lochrie,M. and Gold,L.
    High affinity TGF.beta. nucleic acid ligands and inhibitors
    Patent: US 6346611-A 180 12-FEB-2002;
  JOURNAL
    Location/Qualifiers
    1..34
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match
    100.0%; Score 34; DB 6; Length 34;
  Best Local Similarity
    67.6%; Pred. No. 0.00024;
  Matches
    23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY
  1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
  |||||:::|||||:::|||||:::|||||:::|||||
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34

Db
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34

RESULT 14
  LOCUS
    AR193371
  DEFINITION
    Sequence 181 from patent US 6346611.
  ACCESSION
    AR193371
  VERSION
    AR193371.1 GI:20239336
  KEYWORDS
    '
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 34)
    Pagratia,N., Lochrie,M. and Gold,L.
    High affinity TGF.beta. nucleic acid ligands and inhibitors
    Patent: US 6346611-A 181 12-FEB-2002;
  JOURNAL
    Location/Qualifiers
    1..34
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match
    100.0%; Score 34; DB 6; Length 34;
  Best Local Similarity
    67.6%; Pred. No. 0.00024;
  Matches
    23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY
  1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
  |||||:::|||||:::|||||:::|||||:::|||||
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34

Db
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34
```

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RESULT 15
  LOCUS
    AR193372
  DEFINITION
    Sequence 182 from patent US 6346611.
  ACCESSION
    AR193372
  VERSION
    AR193372.1 GI:20239337
  KEYWORDS
    '
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 34)
    Pagratia,N., Lochrie,M. and Gold,L.
    High affinity TGF.beta. nucleic acid ligands and inhibitors
    Patent: US 6346611-A 182 12-FEB-2002;
  JOURNAL
    Location/Qualifiers
    1..34
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match
    100.0%; Score 34; DB 6; Length 34;
  Best Local Similarity
    67.6%; Pred. No. 0.00024;
  Matches
    23; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY
  1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34
  |||||:::|||||:::|||||:::|||||:::|||||
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34

Db
  1 GGAGGTTATTACAGAGCTGTGTATGCTGTACTCC 34
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Search completed: December 27, 2005, 15:39:56  
Job time : 1988 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: December 27, 2005, 12:44:50 ; Search time 487 Seconds  
(without alignments)  
465.297 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34  
Sequence: 1 ggagguuauacagagucuguaagcugacucc 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn1980a:\*  
2: geneseqn1980a:\*  
3: geneseqn2000a:\*  
4: geneseqn2001a:\*  
5: geneseqn2001b:\*  
6: geneseqn2002a:\*  
7: geneseqn2002b:\*  
8: geneseqn2003a:\*  
9: geneseqn2003b:\*  
10: geneseqn2003c:\*  
11: geneseqn2003d:\*  
12: geneseqn2004a:\*  
13: geneseqn2004b:\*  
14: geneseqn2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	100.0	34	AAF90818	Aaf90818 TGFbeta2
2	34	100.0	34	AAF90873	Aaf90873 NX22284 1
3	34	100.0	34	AAF90877	Aaf90877 NX22284 1
4	34	100.0	34	AAF90796	Aaf90796 TGFbeta2
5	34	100.0	34	AAF90870	Aaf90870 NX22284 1
6	34	100.0	34	AAF90883	Aaf90883 TGFbeta2
7	34	100.0	34	AAF90824	Aaf90824 NX22284 1
8	34	100.0	34	AAF90869	Aaf90869 NX22284 1
9	34	100.0	34	AAF90871	Aaf90871 NX22284 1
10	34	100.0	34	AAF90872	Aaf90872 NX22284 1
11	34	100.0	34	AAF90879	Aaf90879 NX22284 1
12	34	100.0	34	AAF90882	Aaf90882 NX22284 1
13	34	100.0	34	AAF90875	Aaf90875 NX22284 1
14	34	100.0	34	AAF90876	Aaf90876 NX22284 1
15	34	100.0	34	AAF90875	Aaf90875 NX22284 1
16	34	100.0	34	AAF90881	Aaf90881 NX22284 1
17	34	100.0	34	AAF90878	Aaf90878 NX22284 1
18	34	100.0	34	AAF90874	Aaf90874 NX22284 1
19	34	100.0	34	AAF90880	Aaf90880 NX22284 1

20	34	100.0	34	12	AD059385	Ad059385 TGF-beta-
21	34	100.0	34	12	AD059391	Ad059391 Monodonta
22	34	100.0	34	13	AD089377	Ad089377 Human TGF
23	34	100.0	34	13	AD089381	Ad089381 Human TGF
24	34	100.0	34	13	AD089390	Ad089390 Human TGF
25	34	100.0	34	13	AD089376	Ad089376 Human TGF
26	34	100.0	34	13	AD089383	Ad089383 Human TGF
27	34	100.0	34	13	AD089378	Ad089378 Human TGF
28	34	100.0	34	13	AD089382	Ad089382 Human TGF
29	34	100.0	34	13	AD089510	Ad089510 Human TGF
30	34	100.0	34	14	AD089520	Ad089520 Human TGF
31	34	100.0	34	14	AD089525	Ad089525 TGFbeta2-
32	34	100.0	36	5	AAF90795	Aaf90795 TGFbeta2
33	34	100.0	36	5	AAF90817	Aaf90817 TGFbeta2
34	34	100.0	37	5	AAF90819	Aaf90819 TGFbeta2
35	34	100.0	43	5	AAF90794	Aaf90794 TGFbeta2
36	34	100.0	56	5	AAF90793	Aaf90793 TGFbeta2
37	34	100.0	57	5	AAF90792	Aaf90792 TGFbeta2
38	34	100.0	65	13	AD089454	Ad089454 Human TGF
39	34	100.0	70	5	AAF90790	Aaf90790 TGFbeta2
40	34	100.0	82	13	AD089398	Ad089398 Human TGF
41	33	97.1	33	5	AAF90802	Aaf90802 TGFbeta2
42	33	97.1	33	5	AAF90821	Aaf90821 TGFbeta2
43	33	97.1	65	5	AAF90864	Aaf90864 Oligonucle
44	32.4	95.3	70	5	AAF90791	Aaf90791 TGFbeta2
45	32	94.1	32	5	AAF90822	Aaf90822 TGFbeta2

#### ALIGNMENTS

RESULT 1  
AAF90818  
ID AAF90818 standard; RNA; 34 BP.  
XX  
AC AAF90818;  
XX  
DT 03-MAY-2001 (first entry)  
XX  
DE TGFbeta2 ligand 21a-21 truncate #28.  
XX  
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;  
XX systemic evolution of ligands by exponential enrichment; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200109156-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 26-JUL-2000; 2000WO-US020397.  
XX  
PR 29-JUL-1999; 99US-00363939.  
XX  
PA (NEXS-) NEXSTAR PHARM INC.  
XX  
PI Pagratia N, Lochrie M, Gold L;  
XX  
DR WPI; 2001-218217/22.  
XX  
PT New RNA ligand to human transforming growth factor beta2, useful as  
XX pharmaceutical, diagnostics and as immunochemical reagents.  
XX  
PS Claim 1; Page 70; 178pp; English.  
XX  
CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systematic Evolution of Ligands by EXponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention

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XX SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
XX
XX Query Match 100.0%; Score 34; DB 5; Length 34;
XX Best Local Similarity 100.0%; Pred. NO. 4.8e-05;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 2
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ID AAF90873 standard; RNA; 34 BP.
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XX AAF90873;
XX
XX 03-MAY-2001 (first entry)
XX
XX NX22284 ligand variant #6.
XX
XX Human; transforming growth factor beta2; TGFbeta2; SILEX;
XX systemic evolution of ligands by exponential enrichment; ss.
XX
XX Homo sapiens.
XX
XX MO200109156-Al.
XX
XX 08-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US020397.
XX
XX 29-JUL-1999; 99US-00363939.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Pagratia N, Lochrie M, Gold L;
XX
XX WPI; 2001-218217/22.
XX
XX New RNA ligand to human transforming growth factor beta2; useful as
XX pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX
XX Claim 1; Page 78; 178pp; English.
XX
XX The present invention relates to non-naturally occurring, high-affinity
XX RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
XX oligonucleotide ligands were identified by the SELEX method (SELEX stands
XX for Systemic Evolution of Ligands by Exponential Enrichment). The
XX oligonucleotide ligands are useful in any process in which binding to
XX TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
XX diagnostics, imaging agents and immunohistochemical reagents. The present
XX sequence is an oligonucleotide used in the present invention
XX
XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
QY Query Match 100.0%; Score 34; DB 5; Length 34;
Db Best Local Similarity 100.0%; Pred. NO. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 3
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ID AAF90877 standard; RNA; 34 BP.
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XX AAF90877;
XX
XX 03-MAY-2001 (first entry)
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XX Human; transforming growth factor beta2; TGFbeta2; SILEX;
XX systemic evolution of ligands by exponential enrichment; ss.
XX
XX Homo sapiens.
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XX MO200109156-Al.
XX
XX 08-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US020397.
XX
XX 29-JUL-1999; 99US-00363939.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Pagratia N, Lochrie M, Gold L;
XX
XX WPI; 2001-218217/22.
XX
XX New RNA ligand to human transforming growth factor beta2; useful as
XX pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX
XX Claim 1; Page 78; 178pp; English.
XX
XX The present invention relates to non-naturally occurring, high-affinity
XX RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
XX oligonucleotide ligands were identified by the SELEX method (SELEX stands
XX for Systemic Evolution of Ligands by Exponential Enrichment). The
XX oligonucleotide ligands are useful in any process in which binding to
XX TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
XX diagnostics, imaging agents and immunohistochemical reagents. The present
XX sequence is an oligonucleotide used in the present invention
XX
XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
QY Query Match 100.0%; Score 34; DB 5; Length 34;
Db Best Local Similarity 100.0%; Pred. NO. 4.8e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34
Db 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34

RESULT 4
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ID AAF90796 standard; RNA; 34 BP.
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XX AAF90796;
XX
XX 03-MAY-2001 (first entry)
XX
XX TGFbeta2 ligand 21a-21 truncate #6.
XX
XX Human; transforming growth factor beta2; TGFbeta2; SILEX;
XX systemic evolution of ligands by exponential enrichment; ss.
XX
XX Homo sapiens.
XX
XX MO200109156-Al.
XX
XX 08-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US020397.
XX
XX 29-JUL-1999; 99US-00363939.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Pagratia N, Lochrie M, Gold L;
XX
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XX WPI; 2001-218217/22.  
DR New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
PS Claim 1; Page 68; 178pp; English.  
XX  
CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention  
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
  
Query Match 100.0%; Score 34; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34  
  
RESULT 5  
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ID AAF90870 standard; RNA; 34 BP.  
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XX  
DT 03-MAY-2001 (first entry)  
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DE NX22284 ligand variant #3.  
XX  
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KW systemic evolution of ligands by exponential enrichment; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200109156-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 26-JUL-2000; 2000MO-US020397.  
XX  
PR 29-JUL-1999; 99US-00363939.  
XX  
PA (NEXS-) NEXSTAR PHARM INC.  
PI Pagratia N, Lochrie M, Gold L;  
XX WPI; 2001-218217/22.  
XX  
PT New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
XX  
PS Claim 1; Page 78; 178pp; English.  
XX  
CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention  
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34  
DB 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34  
  
RESULT 6  
AAF90883  
ID AAF90883 standard; RNA; 34 BP.  
XX AAF90883;  
XX  
DT 03-MAY-2001 (first entry)  
XX  
DE NX22284 ligand variant #16.  
XX  
KW Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KW systemic evolution of ligands by exponential enrichment; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200109156-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 26-JUL-2000; 2000MO-US020397.  
XX  
PR 29-JUL-1999; 99US-00363939.  
XX  
PA (NEXS-) NEXSTAR PHARM INC.  
PI Pagratia N, Lochrie M, Gold L;  
XX WPI; 2001-218217/22.  
XX  
PT New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
XX  
PS Claim 1; Page 78; 178pp; English.  
XX  
CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention  
SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
  
Query Match 100.0%; Score 34; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34  
DB 1 GGAGGUUUVUACAGAGUCUGUUAUAGCUGUACUCC 34  
  
RESULT 7  
AAF90824  
ID AAF90824 standard; RNA; 34 BP.  
XX AAF90824;  
XX  
DT 03-MAY-2001 (first entry)  
XX  
DE TGFbeta2 ligand 21a-21 truncate #34.  
XX

KW	Human; transforming growth factor beta2; TGFbeta2; SELEX;
KM	systemic evolution of ligands by exponential enrichment; ss.
XX	
OS	Homo sapiens.
PN	MO200109156-A1.
XX	
PD	08-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US020397.
XX	
PR	29-JUL-1999; 99US-00363939.
XX	
PA	(NEXS-) NEXSTAR PHARM INC.
XX	
PI	Pagratis N, Lochrie M, Gold L;
DR	WPI; 2001-218217/22.
XX	
FT	New RNA ligand to human transforming growth factor beta2, useful as
PT	pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX	
PS	Claim 1; Page 70; 178pp; English.
XX	
CC	The present invention relates to non-naturally occurring, high-affinity
CC	RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC	oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC	for Systemic Evolution of Ligands by Exponential Enrichment). The
CC	oligonucleotide ligands are useful in any process in which binding to
CC	TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC	diagnostics, imaging agents and immunohistochemical reagents. The present
CC	invention is an oligonucleotide used in the present invention
SQ	Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;
XX	
Query Match	100.0%; Score 34; DB 5; Length 34;
Best Local Similarity	100.0%; Pred. No. 4.8e-05;
Matches 34; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGAGGUUUA CAGAGUCUGUUA GCGUACUCC 34
DB	1 GGAGGUUUA CAGAGUCUGUUA GCGUACUCC 34
XX	
RESULT 8	
AAF90869	
ID	AAF90869 standard; RNA; 34 BP.
XX	
AC	AAF90869;
XX	
DT	03-MAY-2001 (first entry)
XX	
DE	NX22284 ligand variant #2.
XX	
KM	Human; transforming growth factor beta2; TGFbeta2; SELEX;
KW	systemic evolution of ligands by exponential enrichment; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200109156-A1.
XX	
PD	08-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US020397.
XX	
PR	29-JUL-1999; 99US-00363939.
XX	
PA	(NEXS-) NEXSTAR PHARM INC.
XX	
PI	Pagratis N, Lochrie M, Gold L;
XX	
DR	WPI; 2001-218217/22.
XX	

PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX  
 RESULT 9  
 AAF90871  
 ID AAF90871 standard; RNA; 34 BP.  
 AC AAF90871;  
 XX  
 DT 03-MAY-2001 (first entry)  
 DE NX2284 ligand variant #4.  
 XX  
 KW Human; transforming growth factor beta2, TGFBeta2, SELEX,  
 KW systemic evolution of ligands by exponential enrichment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200109156-A1.  
 PN 08-FEB-2001.  
 PD 26-JUL-2000; 2000WO-US020397.  
 PF 29-JUL-1999; 99US-00363939.  
 PR (NEXS-) NEXSTAR PHARM INC.  
 PA Pagratlis N, Lochrie M, Gold L;  
 PI WPI; 2001-218217/22.  
 DR  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX  
 RESULT 9  
 AAF90871  
 ID AAF90871 standard; RNA; 34 BP.  
 AC AAF90871;  
 XX  
 DT 03-MAY-2001 (first entry)  
 DE NX2284 ligand variant #4.  
 XX  
 KW Human; transforming growth factor beta2, TGFBeta2, SELEX,  
 KW systemic evolution of ligands by exponential enrichment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200109156-A1.  
 PN 08-FEB-2001.  
 PD 26-JUL-2000; 2000WO-US020397.  
 PF 29-JUL-1999; 99US-00363939.  
 PR (NEXS-) NEXSTAR PHARM INC.  
 PA Pagratlis N, Lochrie M, Gold L;  
 PI WPI; 2001-218217/22.  
 DR  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX  
 RESULT 9  
 AAF90871  
 ID AAF90871 standard; RNA; 34 BP.  
 AC AAF90871;  
 XX  
 DT 03-MAY-2001 (first entry)  
 DE NX2284 ligand variant #4.  
 XX  
 KW Human; transforming growth factor beta2, TGFBeta2, SELEX,  
 KW systemic evolution of ligands by exponential enrichment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200109156-A1.  
 PN 08-FEB-2001.  
 PD 26-JUL-2000; 2000WO-US020397.  
 PF 29-JUL-1999; 99US-00363939.  
 PR (NEXS-) NEXSTAR PHARM INC.  
 PA Pagratlis N, Lochrie M, Gold L;  
 PI WPI; 2001-218217/22.  
 DR  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX  
 RESULT 9  
 AAF90871  
 ID AAF90871 standard; RNA; 34 BP.  
 AC AAF90871;  
 XX  
 DT 03-MAY-2001 (first entry)  
 DE NX2284 ligand variant #4.  
 XX  
 KW Human; transforming growth factor beta2, TGFBeta2, SELEX,  
 KW systemic evolution of ligands by exponential enrichment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200109156-A1.  
 PN 08-FEB-2001.  
 PD 26-JUL-2000; 2000WO-US020397.  
 PF 29-JUL-1999; 99US-00363939.  
 PR (NEXS-) NEXSTAR PHARM INC.  
 PA Pagratlis N, Lochrie M, Gold L;  
 PI WPI; 2001-218217/22.  
 DR  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX  
 RESULT 9  
 AAF90871  
 ID AAF90871 standard; RNA; 34 BP.  
 AC AAF90871;  
 XX  
 DT 03-MAY-2001 (first entry)  
 DE NX2284 ligand variant #4.  
 XX  
 KW Human; transforming growth factor beta2, TGFBeta2, SELEX,  
 KW systemic evolution of ligands by exponential enrichment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200109156-A1.  
 PN 08-FEB-2001.  
 PD 26-JUL-2000; 2000WO-US020397.  
 PF 29-JUL-1999; 99US-00363939.  
 PR (NEXS-) NEXSTAR PHARM INC.  
 PA Pagratlis N, Lochrie M, Gold L;  
 PI WPI; 2001-218217/22.  
 DR  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFBeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFBeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 XX  
 Db 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 1 GGAGGUUUVUACAGAGUCUGUAGUCUGUACUCC 34  
 XX

QY 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 10  
AAF90872  
ID AAF90872 standard; RNA; 34 BP.  
XX AAF90872;  
AC  
XX  
DT 03-MAY-2001 (first entry)  
XX  
XX NX22284 ligand variant #5.  
DE  
XX  
XX Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KM systemic evolution of ligands by exponential enrichment; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200109156-A1.  
PN  
XX  
XX 08-FEB-2001.  
PD  
XX  
XX 26-JUL-2000; 2000WO-US020397.  
PF  
XX  
XX 29-JUL-1999; 99US-00363939.  
PR  
XX  
XX (NEXS-) NEXSTAR PHARM INC.  
PA  
XX  
XX Pagratie N, Lochrie M, Gold L;  
PI  
XX  
XX WPI; 2001-218217/22.  
DR  
XX  
XX  
XX New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
XX  
XX Claim 1; Page 78; 178pp; English.

CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by EXponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention

XX  
XX  
XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
SQ

Query Match 100.0%; Score 34; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 11  
AAF90879  
ID AAF90879 standard; RNA; 34 BP.  
XX AAF90879;  
AC  
XX  
DT 03-MAY-2001 (first entry)  
XX  
XX NX22284 ligand variant #12.  
DE  
XX  
XX Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KM systemic evolution of ligands by exponential enrichment; ss.  
XX

OS Homo sapiens.  
XX  
XX WO200109156-A1.  
PN  
XX  
XX 08-FEB-2001.  
PD  
XX  
XX 26-JUL-2000; 2000WO-US020397.  
PF  
XX  
XX 29-JUL-1999; 99US-00363939.  
PR  
XX  
XX (NEXS-) NEXSTAR PHARM INC.  
PA  
XX  
XX Pagratie N, Lochrie M, Gold L;  
PI  
XX  
XX WPI; 2001-218217/22.  
DR  
XX  
XX  
XX New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
XX  
XX Claim 1; Page 78; 178pp; English.

CC The present invention relates to non-naturally occurring, high-affinity  
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
CC for Systemic Evolution of Ligands by EXponential Enrichment). The  
CC oligonucleotide ligands are useful in any process in which binding to  
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
CC diagnostics, imaging agents and immunohistochemical reagents. The present  
CC sequence is an oligonucleotide used in the present invention

XX  
XX  
XX Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
SQ

Query Match 100.0%; Score 34; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34  
DB 1 GGAGGUUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 12  
AAF90882  
ID AAF90882 standard; RNA; 34 BP.  
XX AAF90882;  
AC  
XX  
DT 03-MAY-2001 (first entry)  
XX  
XX NX22284 ligand variant #15.  
DE  
XX  
XX Human; transforming growth factor beta2; TGFbeta2; SELEX;  
KM systemic evolution of ligands by exponential enrichment; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200109156-A1.  
PN  
XX  
XX 08-FEB-2001.  
PD  
XX  
XX 26-JUL-2000; 2000WO-US020397.  
PF  
XX  
XX 29-JUL-1999; 99US-00363939.  
PR  
XX  
XX (NEXS-) NEXSTAR PHARM INC.  
PA  
XX  
XX Pagratie N, Lochrie M, Gold L;  
PI  
XX  
XX WPI; 2001-218217/22.  
DR  
XX  
XX  
XX New RNA ligand to human transforming growth factor beta2, useful as  
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
XX

PS Claim 1, Page 78; 178bp; English.

XX The present invention relates to non-naturally occurring, high-affinity

CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The

CC oligonucleotide ligands were identified by the SELEX method (SELEX stands

CC for Systemic Evolution of Ligands by EXponential Enrichment). The

CC oligonucleotide ligands are useful in any process in which binding to

CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,

CC diagnostics, imaging agents and immunohistochemical reagents. The present

CC sequence is an oligonucleotide used in the present invention

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.8e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 13

AAF90868

ID AAF90868 standard; RNA; 34 BP.

XX

AC AAF90868;

XX

DT 03-MAY-2001 (first entry)

XX

DE NX22284 ligand variant #1.

XX

KM Human; transforming growth factor beta2; TGFbeta2; SELEX;

KW systemic evolution of ligands by exponential enrichment; ss.

XX

OS Homo sapiens.

XX

PN WO200109156-A1.

XX

PD 08-FEB-2001.

XX

PF 26-JUL-2000; 2000WO-US020397.

XX

PR 29-JUL-1999; 99US-00363939.

XX

PA (NEXS-) NEXSTAR PHARM INC.

PI Pagratia N, Lochrie M, Gold L;

DR WPI, 2001-218217/22.

XX

PT New RNA ligand to human transforming growth factor beta2, useful as

PT pharmaceuticals, diagnostics and as immunohistochemical reagents.

PS Claim 1, Page 78; 178bp; English.

XX

CC The present invention relates to non-naturally occurring, high-affinity

CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The

CC oligonucleotide ligands were identified by the SELEX method (SELEX stands

CC for Systemic Evolution of Ligands by EXponential Enrichment). The

CC oligonucleotide ligands are useful in any process in which binding to

CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,

CC diagnostics, imaging agents and immunohistochemical reagents. The present

CC sequence is an oligonucleotide used in the present invention

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.8e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 14

AAF90876

ID AAF90876 standard; RNA; 34 BP.

XX

AC AAF90876;

XX

DT 03-MAY-2001 (first entry)

XX

DE NX22284 ligand variant #9.

XX

KM Human; transforming growth factor beta2; TGFbeta2; SELEX;

KW systemic evolution of ligands by exponential enrichment; ss.

XX

OS Homo sapiens.

XX

PN WO200109156-A1.

XX

PD 08-FEB-2001.

XX

PF 26-JUL-2000; 2000WO-US020397.

XX

PR 29-JUL-1999; 99US-00363939.

XX

PA (NEXS-) NEXSTAR PHARM INC.

PI Pagratia N, Lochrie M, Gold L;

DR WPI, 2001-218217/22.

XX

PT New RNA ligand to human transforming growth factor beta2, useful as

PT pharmaceuticals, diagnostics and as immunohistochemical reagents.

PS Claim 1, Page 78; 178bp; English.

XX

CC The present invention relates to non-naturally occurring, high-affinity

CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The

CC oligonucleotide ligands were identified by the SELEX method (SELEX stands

CC for Systemic Evolution of Ligands by EXponential Enrichment). The

CC oligonucleotide ligands are useful in any process in which binding to

CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,

CC diagnostics, imaging agents and immunohistochemical reagents. The present

CC sequence is an oligonucleotide used in the present invention

XX

SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.8e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

DB 1 GGAGGUUAUACAGAGUCUGUAUAGCUGUACUCC 34

RESULT 15

AAF90875

ID AAF90875 standard; RNA; 34 BP.

XX

AC AAF90875;

XX

DT 03-MAY-2001 (first entry)

XX

DE NX22284 ligand variant #8.

XX

KM Human; transforming growth factor beta2; TGFbeta2; SELEX;

KW systemic evolution of ligands by exponential enrichment; ss.

XX

OS Homo sapiens.

XX

PN WO200109156-A1.

XX 08-FEB-2001.  
 PD  
 XX  
 PF 26-JUL-2000; 2000WO-US020397.  
 XX  
 PR 29-JUL-1999; 99US-00363939.  
 XX  
 PA (NEXS-) NEXSTAR PHARM INC.  
 XX  
 PI Pagratie N, Lochrie M, Gold L;  
 DR WPI; 2001-218217/22.  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 XX pharmaceuticals, diagnostic and as immunochemical reagents.  
 PS Claim 1; Page 78; 178pp; English.  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunochemical reagents. The present  
 CC sequence is an oligonucleotide used in the present invention  
 XX  
 SQ Sequence 34 BP; 8 A; 6 C; 9 G; 0 T; 11 U; 0 Other;  
 Query Match 100.0%; Score 34; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGGUAUUAACAGAGUCUUAUAGCUUAACUCC 34  
 |||||  
 DB 1 GGAGGUAUUAACAGAGUCUUAUAGCUUAACUCC 34

Search completed: December 27, 2005, 15:06:36  
 Job time : 487 secs

***This Page Blank (uspto)***



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 14:30:56 / Search time 3758 Seconds  
(without alignments)  
423.300 Million cell updates/sec

Title: US-10-812-642-115

Perfect score: 34  
Sequence: 1 ggaaguuuacagagucuguuagucguacucc 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.2	65.3	732	7	CR420095 CR420095
2	21.8	64.1	483	9	AQ146760 HS_2241_B
3	21.4	62.9	329	7	CR469204 CR469204
4	21.4	62.9	730	8	CX909337 JGI_CANAL
5	21.4	62.9	769	8	BU747611 CH3#014_B
6	21.4	62.9	772	5	BU415821 60368377
7	21.4	62.9	1209	10	CL043735 CH216-580
8	21.2	62.4	508	9	AQ788713 HS_5549_A
9	21.2	62.4	734	9	BZ055939 11f2401.
10	21.2	62.4	900	10	DU036738 19377 Tom
11	21.2	62.4	1163	8	DN704358 CL152-H09
12	21.1	61.8	533	9	BZ680408 PUBG105TD
13	21.1	61.8	632	10	CZ836446 OC_Ba021
14	21.1	61.8	679	11	CR157585 Forward B
15	21.1	61.8	728	9	AQ258623 nbxb0020N
16	21.1	61.8	977	9	B2394307 E1NCM21TR
17	20.8	61.2	251	1	AV274404 AV274404
18	20.8	61.2	281	5	BX635814 BX635814
19	20.8	61.2	288	1	AA645178 v879a05.r
20	20.8	61.2	319	8	CX200320 MNS01050
21	20.8	61.2	334	3	BM940310 UI-M-CG0P
22	20.8	61.2	381	9	AQ567614 HS_2118_B

23	20.8	61.2	399	1	AI594558	AI594558	uo06g05.Y
24	20.8	61.2	437	2	BE986100	BE986100	UI-M-CG0P
25	20.8	61.2	476	3	BM941736	BM941736	UI-M-CG0P
26	20.8	61.2	480	1	AI592407	AI592407	v879a05.Y
27	20.8	61.2	497	1	AA606330	AA606330	uo06g05.Y
28	20.8	61.2	529	1	AA980547	AA980547	ua42101.r
29	20.8	61.2	543	2	BG946683	BG946683	949013D09
30	20.8	61.2	549	6	CA392086	CA392086	CS21609.Y
31	20.8	61.2	560	5	BX641668	BX641668	DKF2P686J
32	20.8	61.2	565	2	BE290104	BE290104	601089066
33	20.8	61.2	592	3	BT730042	BT730042	603349653
34	20.8	61.2	600	5	BU918118	BU918118	5013-60 M
35	20.8	61.2	600	5	BU918131	BU918131	5013-76 M
36	20.8	61.2	625	7	CK618209	CK618209	m106h09.Y
37	20.8	61.2	653	9	AZ010030	AZ010030	RPCI-23-2
38	20.8	61.2	691	7	CR589375	CR589375	CR589375
39	20.8	61.2	694	2	BG695578	BG695578	NISC_1v19
40	20.8	61.2	737	10	CZ850894	CZ850894	OC_Ba023
41	20.8	61.2	755	8	CX210472	CX210472	MNS29414
42	20.8	61.2	767	2	BF169054	BF169054	601773331
43	20.8	61.2	791	6	CB952424	CB952424	AGENCOURT
44	20.8	61.2	848	7	CK847093	CK847093	969680 MA
45	20.8	61.2	1482	4	AK079249	AK079249	Mus muscu

#### ALIGNMENTS

RESULT 1  
LOCUS CR420095/c 732 bp mRNA linear EST 17-JUN-2004  
DEFINITION CR420095 XGC-tailbud Xenopus tropicalis cDNA clone TTBA067g23 5',  
mRNA sequence.  
ACCESSION CR420095  
VERSION CR420095.1 GI:48913503  
KEYWORDS EST.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis

REFERENCE  
AUTHORS Crompton,M.D.R., Ahnurst,J.L., Taylor,R., Garrett,N. and Rogers,J.  
TITLE Sanger Xenopus tropicalis EST project 2001 (2004)  
JOURNAL Unpublished (2004)  
COMMENT Contact: Crompton MDR  
Sanger Institute  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk

FEATURES  
source  
1..732  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="TTBA067g23"  
/dev\_stage="tailbud (stage 28-30)"  
/lab\_host="Escherichia coli DH10B."  
/clone\_1lb="XGC-tailbud"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; CDNA was oligo dt primed from 5ug of poly A+ RNA from tailbud. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

#### ORIGIN

Query Match 65.3%; Score 22.2; DB 7; Length 732;  
Best Local Similarity 51.9%; Pred. No. 1.6e+02;  
Matches 14; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 6 UNANUACAGAGUCUGUAGUCUGUACU 32  
 Db 182 TTATTCAGAGCTCTGTCTACTGTAACCT 156

RESULT 2  
 A0146760 483 bp DNA linear GSS 08-OCT-1998  
 A0146760/c  
 LOCUS HS 2241 B2 D03 MR CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION sapiens genomic clone Plate=2241 Col=6 Row=H, genomic survey  
 sequence.

ACCESSION A0146760  
 VERSION A0146760.1 GI:3537413  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 483)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Koller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 10449764

TITLE Contact: Mahairas GG, Wallace JC, Hood L  
 JOURNAL High Throughput Sequencing Center  
 PUBMED University of Washington  
 COMMENT 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 2241 row: H column: 6  
 Class: BAC ends  
 High quality sequence stop: 483.  
 Location/Qualifiers  
 1. 483  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=2241 Col=6 Row=H"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /note="Organ: sperm; Vector: pBelbac11; BAC clones in  
 E-Coli DH10B"

ORIGIN

Query Match 64.1%; Score 21.8; DB 9; Length 483;  
 Best Local Similarity 56.0%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GUNANUACAGAGUCUGUAGUCUGUAC 29  
 Db 193 GTCATTCACAGCTCTGTACTAGTGT 169

RESULT 3  
 CR469204 329 bp mRNA linear EST 01-JUL-2004  
 LOCUS CR469204 Rat pBluescript Lion Rattus norvegicus cDNA clone  
 DEFINITION LIONP463B08404 3', mRNA sequence.  
 ACCESSION CR469204  
 VERSION CR469204.1 GI:49601553  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
 1 (bases 1 to 329)

REFERENCE

AUTHORS Heinrich,J., Hermann,J., Kranz,H., Loebbert,R., Schlueker,T.,  
 Schette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,  
 Radloff,U., Schneider,D. and Korn,B.  
 Rat ArrayTAG CDNA  
 Unpublished (2004)  
 COMMENT Contact: Inge Arltart  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Email: www.rzpd.de  
 RZPD: LIONP463B08404.  
 RZPDLIB:  
 Rat ArrayTAG CDNA  
 http://www.rzpd.de/cgi-  
 bin/products/showlib.pl.cgi?response?libNo=463 Contact: Inge Arltart  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 100  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 RP: CAGGAACAGCTATGAC.

FEATURES  
 source  
 1. 329  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="LIONP463B08404"  
 /lab\_host="DH10B"  
 /clone\_lib="Rat pBluescript Lion"

ORIGIN

Query Match 62.9%; Score 21.4; DB 7; Length 329;  
 Best Local Similarity 58.1%; Pred. No. 3.2e+02;  
 Matches 18; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGAGUNUACAGAGUCUGUAGUCUGUAC 31  
 Db 195 GGAGTTACTACAAAGTCTGTACGCTTAC 165

RESULT 4  
 CX909337 730 bp mRNA linear EST 04-AUG-2005  
 LOCUS UGI CAAN1789.rev NIH XGC troypt4 Xenopus tropicalis cDNA clone  
 DEFINITION IMAGE:7687386 3', mRNA sequence.  
 ACCESSION CX909337  
 VERSION CX909337.2 GI:71830453  
 KEYWORDS EST.  
 SOURCE Xenopus tropicalis (western clawed frog)  
 ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;  
 Xenopodinae; Xenopus; Silurana.  
 1 (bases 1 to 730)  
 Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,  
 Brokstein,P. and Lindquist,E.A.  
 DOE Joint Genome Institute Xenopus tropicalis EST project  
 Unpublished (2004)  
 Other\_ESTs: UGI\_CAAN1789.fwd  
 Contact: Lindquist,E.A., Richardson,P.  
 DOE Joint Genome Institute  
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 Tel: 925 296 5600  
 Fax: 925 296 5710  
 Email: cdna@jgi-psf.org  
 Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,  
 University of California, Berkeley)  
 http://tropicalis.berkeley.edu/home/  
 cDNA Library Preparation: DOE Joint Genome Institute:  
 http://www.jgi.doe.gov  
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/ILNLT:  
 http://image.llnl.gov  
 Naming Convention: EST name is generated by the concatenation of  
 the JGI Clone Id and the direction of sequencing. The suffix '.rev'  
 necessarily reflect the orientation of the insert. It does not  
 necessarily reflect the orientation of the insert.  
 Plate: CANAN 0017 row: 1 column: 16  
 High quality sequence stop: 725  
 POLY-A=yes.

#### FEATURES

source

Location/Qualifiers  
 1. 730  
 /organism="Xenopus tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="IMAGE:7687386"  
 /sex="male"  
 /tissue\_type="Testes"  
 /dev\_stage="Adult"  
 /lab\_host="ElectroMAX DH10B"  
 /clone\_lib="NIH XGC triopte4"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 This library was made from dt primed cDNA and cloned into  
 Invitrogen pCMVSPORT6 vector. The work was done at DOE  
 Joint Genome Institute. Poly A RNA were primed with 5'  
 GACTAGTCTAGATCGCAG CGCCGCCCTTTTCTTTTCTTTT 3'. cDNA  
 were ligated to SalI adapter (5' TCGACCGACGCGCG and  
 5'CGGACGCGTGGG) digested with NotI, size fractionated in  
 1.1% agarose gel electrophoresis and ligated into NotI and  
 SalI digested pCMVSPORT6 vector."

#### ORIGIN

Query Match 62.9%; Score 21.4; DB 8; Length 730;  
 Best Local Similarity 45.2%; Pred. No. 3.6e+02;  
 Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 GAGGUUAVUACAGAGUCUGUAGUCUGUAC 32  
 ||::||:|::||:|::||:|::||:|:  
 Db 255 GAGTTATTTCAGTGTCTGTTAGATGATT 285

RESULT 5 769 bp mRNA linear EST 10-OCT-2002  
 BU747611  
 LOCUS CH3#014\_B02T7 Canine heart normalized cDNA library in pBluescript  
 DEFINITION Canis familiaris cDNA clone CH3#014\_B02 5', mRNA sequence.  
 ACCESSION BU747611  
 VERSION BU747611 GI:23698691  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.  
 1 (bases 1 to 769)  
 YI.Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.  
 Expressed sequence tags from Canine heart  
 Unpublished (2003)  
 Other\_FEATURES: CH3#014\_B02T7  
 Contact: George AL  
 Division of Genetic Medicine  
 Vanderbilt University  
 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
 Tel: 615 936 2660  
 Fax: 615 936 2661  
 Email: al.george@vanderbilt.edu  
 Seq primer: T7: TATACACTACTATAGCG  
 High quality sequence start: 176  
 High quality sequence stop: 435.  
 Location/Qualifiers  
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 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

#### FEATURES

source

1. 769  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"

/clone="CH3#014\_B02"  
 /tissue\_type="heart"  
 /cell\_type="heart"  
 /dev\_stage="mixed developmental stages (adult, 30 day - 40  
 day fetal)"  
 /clone\_lib="Canine heart normalized cDNA library in  
 pBluescript"  
 /note="Organ: heart; Vector: pBluescript; Site 1: 5' of  
 vector NotI; Site 2: 3' of vector EcoRI; Tissue source:  
 dog heart (adult, 30 day - 40 day fetal), right and left  
 atria and ventricle. Dog breed - mixed (beagle, German  
 shepherd, pointer, Irish setter). Library construction:  
 oligo-dT primed"

#### ORIGIN

Query Match 62.9%; Score 21.4; DB 5; Length 769;  
 Best Local Similarity 45.2%; Pred. No. 3.6e+02;  
 Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 3 AGGUUAVUACAGAGUCUGUAGUCUGUAC 33  
 ||::||:|::||:|::||:|::||:|:  
 Db 689 AGGTTATTTCAGTGTCTGTTAGTGTCTC 659

RESULT 6 772 bp mRNA linear EST 29-NOV-2002  
 BU415821  
 LOCUS 60366937F1 CSEORBL06 Gallus gallus cDNA clone CHEST61119 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU415821  
 VERSION BU415821.1 GI:25908492  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 772)  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 12445392  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

#### FEATURES

source

Location/Qualifiers  
 1. 772  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST61119"  
 /sex="Male and female"  
 /tissue\_type="Abdominal fat pad"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEORBL06"  
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
 Site 2: NotI; Modification of pBluescript II KS(+)  
 (Stratagene) vector to accommodate cDNA produced with the  
 T-primed protocol (Construction of uni-directionally  
 cloned cDNA libraries from messenger RNA for improved 3'  
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
 Ligate in double stranded adaptor containing BspI and  
 BamHI sites (5'ggccgctgcagcccgatccgaaataag)  
 (5'aattcttttcgataccgggctcgcagc)"

```

ORIGIN
Query Match      62.9%; Score 21.4; DB 5; Length 772;
Best Local Similarity 45.2%; Pred. No. 3.6e+02;
Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Oy      4 GGUUAUACAGAGUCUGUAGCUGUACUCC 34
      ||::|||::|||::|||::|||::|||
Db      685 GGTATTATAGTGTCTGTATATCTGTATCTGC 715

RESULT 7
LOCUS      CL043735      1209 bp      DNA      linear      GSS 03-DEC-2003
DEFINITION  CH216-5808 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-5808,
              genomic survey sequence.
ACCESSION  CL043735
VERSION    CU043735.1 GI:40499648
KEYWORDS   GSS.
SOURCE     Xenopus tropicalis (western clawed frog)
ORGANISM   Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
            1 (bases 1 to 1209)
            Kremnitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
            A physical map of the xenopus tropicalis genome
            Unpublished (2003)
            Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submls@wustl.edu
            Insert Length: 175000 Std Error: 0.00
            Seq primer: SP6 ATTAGGTGACACTATAG
            Class: BAC ends
            High quality sequence start: 19
            High quality sequence stop: 631.
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                /db_xref="taxon:8364"
                /clone="CH216-5808"
                /sex="male"
                /cell_line="Stock 248 F7A2, inbred N7"
                /clone_lib="CH216"
                /note="Vector: pTARAC2.1, CHORI-216 Xenopus tropicalis
                BAC library"

ORIGIN
Query Match      62.9%; Score 21.4; DB 10; Length 1209;
Best Local Similarity 45.2%; Pred. No. 3.9e+02;
Matches 14; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Oy      2 GAGGUUAUACAGAGUCUGUAGCUGUACU 32
      ||::|||::|||::|||::|||::|||
Db      285 GATGTATTTCAGTGTCTGTATATCTGTATT 315

RESULT 8
LOCUS      A0788713      508 bp      DNA      linear      GSS 03-AUG-1999
DEFINITION  HS_5549_A1_H02_T7A RPCI-11 Human Male BAC Library Homo sapiens
              genomic clone Plate=1125 Col=3 Row=0, genomic survey sequence.
ACCESSION  A0788713
VERSION    A0788713.1 GI:5696337
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

```

REFERENCE      1 (bases 1 to 508)
AUTHORS       Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
              Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
              Hood,L.
              Sequence-tagged connectors: A sequence approach to mapping and
              scanning the human genome
              Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
              10449764
JOURNAL       PubMed
COMMENT       Contact: Mahairas GG, Wallace JC, Hood L
              High Throughput Sequencing Center
              University of Washington
              401 Queen Anne Avenue North, Seattle, WA 98109, USA
              Tel: (206) 616-3618
              Fax: (206) 616-3887
              Email: jwallace@u.washington.edu
              Clones are derived from the human BAC library RPCI-11. For BAC
              library availability, please contact Pieter de Jong
              (pieter@dejong.med.buffalo.edu). Clones may be purchased from
              BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
              or from Resear h Genetics (info@resgen.com). BAC end Web Server:
              http://www.htseq.washington.edu
              plate: 1125 row: 0 column: 3
              Seq primer: T7
              Class: BAC ends
              High quality sequence stop: 508.
              Location/Qualifiers
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                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /clone="Plate=1125 Col=3 Row=0"
                  /sex="male"
                  /clone_lib="RPCI-11 Human Male BAC Library"
                  /note="Vector: pBAC3.6; Site 1: EcoRI, Site 2: EcoRI;
                  Male blood DNA was isolated from one randomly chosen donor
                  and partially digested with a combination of EcoRI and
                  EcoRI Methylase. Size selected DNA was cloned into the
                  pBAC3.6 vector at EcoRI sites"

ORIGIN
Query Match      62.4%; Score 21.2; DB 9; Length 508;
Best Local Similarity 61.5%; Pred. No. 4.1e+02;
Matches 16; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy      3 AGGUUAUACAGAGUCUGUAGCUG 28
      ||::|||::|||::|||::|||
Db      471 AGGTATTACAGTCTGTATTACAG 446

RESULT 9
LOCUS      BZ055939      734 bp      DNA      linear      GSS 09-OCT-2002
DEFINITION  11f26d01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
              sequence.
ACCESSION  BZ055939
VERSION    BZ055939.1 GI:23660972
KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 734)
            Delehaunty,K., Fowell,G., Fulton,L., McComble,W.R., Miner,T.,
            Nash,W., Radhnowicz,P.D. and Wilson,R.K.
            Whole genome shotgun reads from Brassica oleracea
            Unpublished (2002)
            Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submls@wustl.edu
            Plate: 11f26 row: d column: 01

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OY	1	GGAGGUAUUAACAGAGUCUGUAUAGCUGUACCC	34
Db	952	GGGTTTATTAAGAAGCGCTGTTCGCTTACTGCC	985
RESULT 12			
BZ680408		533 bp	DNA
LOCUS	PUBG10STD ZM 0.6 1.0 KB	Zea mays genomic clone ZMMBT049A09,	linear GSS 05-FEB-2003
DEFINITION	genomic survey sequence.		
ACCESSION	BZ680408		
VERSION	BZ680408.1	GI:28235276	
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 533) WhiteLaw,C.A., Quackenbush,J.J., Van Aken,S., Utechtack,T., Bennerick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerckren,J.		
TITLE	Maize Genomics Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Cathy WhiteLaw TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whiteLaw@cigr.org Seq primer: TP Class: sheared ends.		
FEATURES	Location/Qualifiers		
source	1..533 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBT049A09" /clone_1ib="ZM 0.6 1.0 KB" /note="Vector: pCR4-ToPO, Site 1: EcoRI, 0.6-1.0 kb high Cot selected genomic DNA library"		
ORIGIN			
Query Match	61.8%; Score 21; DB 9; Length 533;		
Best Local Similarity	48.3%; Pred. No. Se+02;		
Matches	14; Conservative 10; Mismatches 5; Indels 0; Gaps 0;		
OY	2	GAGGUUAUUAACAGAGUCUGUAUAGCUGUA	30
Db	30	GAGTTTGTTACGAGAGTCGTGTTGCTGA	58
RESULT 13			
CZ836446		632 bp	DNA
CZ836446	OC_Ba021P12.r OC_Ba	Oryza coarctata genomic clone OC_Ba021P12	linear GSS 27-JUL-2005
DEFINITION	3', genomic survey sequence.		
ACCESSION	CZ836446		
VERSION	CZ836446.1	GI:71289972	
KEYWORDS	GSS.		
SOURCE	Oryza coarctata (Porteresia coarctata)		
ORGANISM	Oryza coarctata		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.		
AUTHORS	1 (bases 1 to 632) Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D., Rao,K., Luo,M., Jety,R., Kudrna,D., Muller,C., Soderlund,C. and Weng,R.		
TITLE	OMP (Oryza Map Alignment Project) - Arizona Genomics Institute		

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JOURNAL      Unpublished (2005)
COMMENT       Contact: Rod A. Wing
              Arizona Genomics Institute
              University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9595
              Fax: 520 621 1259
              Email: rwing@genome.arizona.edu
PCR Primers   FORWARD: TAA TAC GAC TCA CTA TAG GG
              BACKWARD: CAC TCA TTA GGC ACC CCA
              Plate: 0219 row= P column= 12
              Seq primer: CAC TCA TTA GGC ACC CCA
              Class: BAC ends.
FEATURES       Location/Qualifiers
Source         1..632
               /organism="Oryza coarctata"
               /mol_type="genomic DNA"
               /db_xref="taxon:77588"
               /clone="OC_Ba0219P12"
               /tissue_type="leaves"
               /dev_stage="mature"
               /lab_host="DH10B"
               /clone_1fb="OC_Ba"
               /note="vector: pGAD1AC1; site_1: HindIII; site_2: HindIII"
ORIGIN
Query Match   61.8%; Score 21; DB 10; Length 632;
Best Local Similarity 48.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY            6 UUAUACAGAGUCUGUAVAGCUGAACCC 34
             ::::|::|::|::|::|::|::|::|
Db            380 TTATTACTGATGTATAGCAATACTCC 408

RESULT 14
LOCUS        CR157585                679 bp          DNA           linear    GSS 06-JUN-2004
DEFINITION   Forward strand read from insert in 5'HPRT insertion targeting and
              chromosome engineering clone MHPN356123, genomic survey sequence.
ACCESSION    CR157585
KEYWORDS     GGS; genome survey sequence; MICER.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 679)
AUTHORS      Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
              Jonkers,D., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
              Rogers,J. and Bradley,A.
TITLE        Direct Submission
JOURNAL      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES     Location/Qualifiers
Source       1..679
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /db_xref="taxon:10090"
              /clone="MHPN356123"
              /clone_1fb="MHPN"
ORIGIN
Query Match   61.8%; Score 21; DB 11; Length 679;
Best Local Similarity 51.7%; Pred. No. 5.2e+02;
Matches 15; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY            6 UUAUACAGAGUCUGUAVAGCUGAACCC 34
             ::::|::|::|::|::|::|::|::|
Db            215 TTATGACAAGTCAGTATGGCTGACTGCC 243

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## RESULT 15

AQ258623

LOCUS

DEFINITION

AQ258623 728 bp DNA linear GSS 23-OCT-1998  
 nbxb0020N10F CUGI Rice BAC library Oryza sativa (japonica  
 cultivar-group) genomic clone nbxb0020N10F, genomic survey  
 sequence.

ACCESSION

AQ258623.1 GI:3793105

VERSION

GSS.

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriactoidae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 728)  
 Wing, R.A. and Dean, R.A.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1998)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Seq primer: TATATGACCTCCTATAGCG

Class: BAC ends

High quality sequence stop: 241.

## FEATURES

source

Location/Qualifiers

1..728

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/cultivar="japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="nbxb0020N10F"

/issue\_type="leaf"

/lab\_host="E. coli DH10B"

/clone\_id="CUGI Rice BAC library"

/note="Vector: pBelOAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

## ORIGIN

Query Match

61.8%; Score 21; DB 9; Length 728;

Best Local Similarity

48.3%; Pred. No. 5.3e+02;

Matches 14; Conservative

10; Mismatches 5; Indels 0; Gaps 0;

Oy

6 UUAUACAGAGUCGUUAUACGCUAUCGC 34

Db

381 TTTTACTGAGCTATATAGACGTACTCC 409

Search completed: December 27, 2005, 16:42:52  
 Job time : 3764 secs

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